

Derivation of the code for amino acids

For the average proportions of amino acids (Cf. Atlas of protein sequence and structure, loc. cit.: Gly = 8,4%, Ala = 8,6%, Ser = 7,0%, Pro+Val+Thr+Cys = 20,8%, Leu+Ile+Asn+Asp = 21,7%, Gln+Lys+Glu+Met = 18,2%, His = 2,0%, Phe = 3,6%, Arg+Tyr = 8,3%, Trp = 1,3%), the global harmonic distance (computed over all the possible pairs of frequencies after synchronization, i. e. over 100 pairs in the case the synchronization results in 10 different notes), as given by the quoted formula (that is  $8.4 \times 8.6 \times \text{Log} 6 + 8.4 \times 7.0 \times \text{Log} 3 + 8.4 \times 20.8 \times \text{Log} 8 + 8.4 \times 21.7 \times 2 \times \text{Log} 9 + 8.4 \times 18.2 \times \text{Log} 2 + 8.4 \times 2.0 \times \text{Log} 32 + \dots$ , sum of 100 terms), is minimal (among different neighbouring choices of synchronization values) for the ratios of frequencies in ascending order (starting from Gly = 1):  
1, 6/5, 3/2, 8/5, 9/5, 2, 32/15, 9/4, 12/5, 8/3  
giving the following frequencies (from Gly = 220 Hz on):  
220, 264, 330, 352, 396, 440, 469.33, 495, 528, 586.67 Hz  
corresponding to the notes  
low A, C, E, F, G, A, B flat, B, high C, high D  
i. e. to within the approximation of the chromatic tempered scale  
(i.e.  $220 \times$  times an integer power of  $2^{1/12}$ ):  
220, 262, 330, 349, 392, 440, 466, 494, 523, 587 Hz  
or in the inhibition case:  
262, 294, 311, 330, 349, 392, 440, 466, 587, 698 Hz  
corresponding to the notes  
C, D, E flat, E, F, G, B flat, high D, high F  
as claimed.

In cells where the proportions of transfer RNAs (and hence of amino acids) differ from the average, the frequencies may differ slightly from the frequencies on the first line above, but to within the approximation of the chromatic tempered scale, the result has remained unchanged in the some 1000 genes so far transposed according to the method of the present invention. An elementary probabilistic computation (knowing there are about 100 000 genes in the genome) enables one to deduce that the same result must be true for at least 99% of the genes, therefore it has been termed 'universal' (however, exceptions for the last 1% are not excluded).

- % dans les positions: 8.4 8.6 7.0 20.8 21.7 18.2 3.6 8.3 1.3  
 nb codons (chaî 64): 4 4 6 14 13 7 2 2 8 1

h \ d	d	G	A	S	PV TC	LI ND	QK EM	H	F	RY	W
		0	1	2	3	4	5	6	7	8	9
G - Gly	0	0	1	2	3	4	5	6	7	8	9
A - Ala	1	Log 6	0	1	2	3	4	5	6	7	8
S - Ser	2	Log 3	Log 5	0	1	2	3	4	5	6	7
P-Pro V-Val T-Thr C-Cys	3	Log 8	Log 4	Log 16	0	1	2	3	4	5	6
L-Leu I-Ile N-Asn D-Asp (B-Asx)	4	Log 9	Log 3	Log 6	Log 9	0	1	2	3	4	5
Q-Gln K-Lys E-Glu H-Het (Z-Grx)	5	Log 2	Log 5	Log 4	Log 5	Log 10	0	1	2	3	4
H - His [6] [54] [21]	6	Log 32	Log 16	Log 64	Log 4	Log 32	Log 16	0	1	2	3
F - Phe [50C]	7	Log 9	Log 15	Log 3	Log 45	Log 5	Log 9	Log 135	0	1	2
R - Arg Y-Tyr	8	Log 12	Log 2	Log 8	Log 3	Log 4	Log 6	Log 9	Log 16	0	1
W - Trp [6]	9	Log 8	Log 20	Log 16	Log 5	Log 40	Log 4	Log 5	Log 32	Log 10	0

Homma  
 E. G. li

Distances mélodiques (d) et harmoniques (h) entre peptides (acides aminés)

$\langle d \rangle = 3,30 \pm 2,380476$  Avec multiplicité:  $2,525 \pm 1,979441145$   
 $\langle h \rangle = \pm 1,717498089 \pm 0,9954023322$  [6: 1,732061204]  
 $\sigma_d / \sigma_h = 1,352834391$

$\delta = \left( \bar{d} + \left( \frac{\sigma_d}{\sigma_h} \right)^2 \bar{h} \right) / \left( 1 + \left( \frac{\sigma_d}{\sigma_h} \right)^2 \right)$   $\bar{d} = d / \langle d \rangle, \bar{h} = h / \langle h \rangle$

$\mu = 100(1 - \delta)$  niveau musical

$\theta$	$1$	$2$	$3$	$4$	$5$	$6$	$7$	$8$	$9$
$\alpha$	$\alpha_0$	$\alpha_1$	$\alpha_2$	$\alpha_3$	$\alpha_4$	$\alpha_5$	$\alpha_6$	$\alpha_7$	$\alpha_8$
1	$\frac{6}{5}$	$\frac{3}{2}$	$\frac{8}{5}$	$\frac{9}{5}$	2	$\frac{32}{15}$	$\frac{9}{4}$	$\frac{12}{5}$	$\frac{8}{3}$
5	1	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{3}{2}$	$\frac{5}{3}$	$\frac{16}{9}$	$\frac{15}{8}$	2	$\frac{20}{9}$
3	$\frac{5}{4}$	1	$\frac{16}{15}$	$\frac{6}{5}$	$\frac{4}{3}$	$\frac{64}{15}$	$\frac{3}{2}$	$\frac{8}{5}$	$\frac{16}{9}$
2	$\frac{4}{3}$	$\frac{16}{15}$	1	$\frac{9}{8}$	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{45}{32}$	$\frac{3}{2}$	$\frac{5}{3}$
9	$\frac{5}{4}$	$\frac{6}{5}$	$\frac{9}{8}$	1	$\frac{10}{9}$	$\frac{32}{15}$	$\frac{5}{4}$	$\frac{4}{3}$	$\frac{16}{9}$
2	$\frac{5}{3}$	$\frac{4}{3}$	$\frac{5}{4}$	$\frac{10}{9}$	1	$\frac{16}{15}$	$\frac{9}{8}$	$\frac{6}{5}$	$\frac{5}{3}$
3	$\frac{16}{15}$	$\frac{6}{5}$	$\frac{4}{3}$	$\frac{3}{2}$	$\frac{16}{15}$	1	$\frac{15}{128}$	$\frac{9}{8}$	$\frac{5}{4}$
9	$\frac{5}{4}$	$\frac{3}{2}$	$\frac{4}{3}$	$\frac{5}{4}$	$\frac{9}{8}$	$\frac{19}{128}$	1	$\frac{16}{15}$	$\frac{32}{27}$
5	2	$\frac{8}{5}$	$\frac{3}{2}$	$\frac{5}{4}$	$\frac{6}{5}$	$\frac{9}{8}$	$\frac{16}{15}$	1	$\frac{10}{9}$
3	$\frac{2}{3}$	$\frac{16}{9}$	$\frac{5}{3}$	$\frac{4}{3}$	$\frac{4}{3}$	$\frac{5}{4}$	$\frac{32}{27}$	$\frac{10}{9}$	1

Per. de la 19<sup>me</sup>  
(Cavendish 1914)

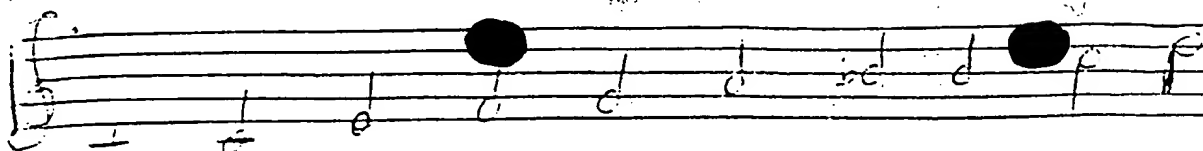
1,80875  
(1,77409)  
1,66651  
(1,48206) -  
1,87682 -  
(1,73478)  
1,79460  
(1,46830)  
1,97378 -  
(1,73119)  
1,57488  
(1,46132)  
2,67338  
(2,10004)  
2,47608  
(1,19887)  
1,68066  
(1,48183) -  
2,19101 -  
(1,11771)

$\langle h \rangle = 1,97165$

over 60  
multiplicity

CALCUL DE LA DISTANCE HARMONIQUE GLOBALE

15482  
13113  
164  
175  
157  
225  
241  
262  
275



Do 1 2 3 4 5 6 7 8 9

G-Gly A-Ala S-Ser P-Pro L-Leu Q-Gln H-His F-Phe R-Arg W-Trp  
 V-Val I-Ileu K-Lys Y-Tyr  
 T-Thr N-Asn E-Glu  
 C-Cys D-Asp M-Met

Ln	Symbol	Mass	Name	Abundance (%)	Multiplicity (Ratio)	Notes
224	G - Gly	75, 37	La 220	0.53 0.81 2, 4 (+18)	4 (GAX)	Glycine La + 1/6
266	A - Ala	89, 40	Do 262	1.45 0.97 8, 6 (+2)	4 (GAX)	Alanine Do + 1/6
313	S - Ser	105, 40	Mi (b) 330	0.79 0.72 7, 2 (-28)	[98] 6 (GAX, AGA)	Serine Mi b + 1/12
343	P - Pro	118, 14	Fa (-) 349	0.59 0.62 5, 2 (-14)	[66] 4 (GAX)	Proline Fa - 1/8
349	V - Val	117, 18	Fa "	1.14 1.65 6, 6 (=)	4 (GAX)	Valine Fa
355	T - Thr	119, 12	Fa "	0.82 1.20 6, 1 (-20, 5)	4 (GAX)	Threonine Fa + 1/6
361	C - Cys	121, 16	Fa (#-) "	0.77 1.30 2, 9 (-24)	2 (GAX)	Cysteine Fa + 1/3
391	L - Leu	131, 18	Sb 392	1.34 1.22 7, 4 (-24)	6 (GAX, IER)	Leucine Sb
391	I - Ile	131, 18	Sb "	1.20 1.60 4, 5 (-20, 4)	[42] 3 (ATG, ATA)	Isoleucine Sb
394	N - Asn	132, 12	Sb "	0.73 0.65 4, 3 (-20)	2 (GAY)	Asparagine Sb + 1/12
397	D - Asp	133, 11	Sb "	0.78 0.80 5, 5 (-22)	[33] 2 (GAY)	Aspartic acid Sb - 1/6
436	Q - Gln	146, 15	La 460	1.17 1.23 3, 9 (-20, 0)	2 (CAR)	Glutamine La
436	K - Lys	146, 19	La "	1.27 0.74 6, 6 (-20, 3)	2 (AAR)	Lysine La
439	E - Glu	147, 14	La "	1.53 0.26 6, 6 (-20, 3)	2 (GAR)	Glutamic acid La
445	M - Met	149, 22	La "	1.20 1.67 1, 7 (-20, 2)	1 (ATG)	Methionine La + 1/6
463	H - His	155, 16	Sb 466	1.24 0.71 2, 2 (-18)	2 (GAY)	Histidine Sb
492	F - Phe	165, 20	Si 494	1.12 1.28 3, 6 (-20, 3)	2 (TRY)	Phenylalanine Si
513	R - Arg	174, 24	Do 523	0.77 0.70 4, 9 (-20, 2)	6 (GAX, AGR)	Arginine Do
540	Y - Tyr	181, 26	Do (#-) "	0.67 1.27 2, 4 (-20, 2)	2 (GAY)	Tyrosine Do + 1/3
605	W - Trp	204, 23	Re (#-) 587	1.14 1.19 1, 7 (-20, 3)	[16] 1 (TGG)	Tryptophan Re + 1/3

[1.0000 = 2,98094 H<sub>2</sub> mass 26.02558]

[Y: 1.00000 = 1.00000 T: 1.00000  
 R: 1.00000 = 1.00000 A: 1.00000]

A	B	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	X	Y	Z
1	4	3	4	5	4	0	6	4	5	4	5	4	3	5	2	2	3	3	9	8		(5)
Do	La	Do	La	Si	La	Sb	La	La	La	La	La	La	La	Do	Mi	Fa	Fa	Re	Do	La		
1	5	4	3	5	7	6	7	5	6	5	6	5	6	7	3	4	4	2	1	6		mass 2
Ala	Arg	Asn	Asp	Cys	Glu	Gln	Gly	His	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Trp	Tyr	Val			
1	2	4	4	3	5	5	0	6	4	4	5	5	7	3	2	3	9	8	3			
Do	La	Do	La	Fa	La	La	La	Sb	Sb	Sb	La	La	Si	Fa	Mi	Fa	Re	Do	Fa			

Mod. 2 142

